

SEQUENCE LISTING

<110> Japan Tobacco, Inc.

<120> Monoclonal Antibody Against Connective Tissue Growth Factor  
and Medicinal Uses Thereof

<130> J1-009PCT

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<150> JP P1997-367699

<151> 1997-12-25

<150> JP P1998-356183

<151> 1998-12-15

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<170> PatentIn Ver. 2.0

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<211> 2338

<212> DNA

<213> Rat

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<221> 5'UTR

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<221> CDS

<222> (213)...(1256)

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<222> (1257)...(2338)

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<221> polyA\_signal

<222> (2297)...(2302)

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accaaacctcc gccccgagac cgagtccagg ctccggccgc gcccctcgac gcctctgcac 180

cccgctgtgc gtcctcctgc cgcgccccga cc atg ctc gcc tcc gtc gcg ggt 233

Met Leu Ala Ser Val Ala Gly

1 5

ccc gtt agc ctc gcc ttg gtg ctc ctc tgc acc cgg cct gcc acc 281

Pro Val Ser Leu Ala Leu Val Leu Leu Leu Cys Thr Arg Pro Ala Thr

10

15

20

ggc cag gac tgc agc gcg cag tgt cag tgc gca cgt gaa gcg gcg ccg		329	
Gly Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Arg Glu Ala Ala Pro			
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cgc tgc ccc gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc		377	
Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys			
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cgc gtc tgc gcc aag cag ctg gga gaa ctg tgc acg gag cgt gat ccc		425	
Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro			
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tgc gac cca cac aag ggt ctc ttc tgc gac ttc ggc tcc ccc gcc aac		473	
Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn			
75	80	85	
cgc aag att ggc gtg tgc cct gcc aaa gat ggt gca ccc tgt gtc ttc		521	
Arg Lys Ile Gly Val Cys Pro Ala Lys Asp Gly Ala Pro Cys Val Phe			
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ggt ggg tcc gtg tac cgc agc ggc gag tcc ttc caa agc agt tgc aaa		569	
Gly Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys			
105	110	115	
tac cag tgc act tgc ctg gat ggg gcc gtg ggc tgt gtg ccc ctg tgc		617	
Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys			
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agc atg gac gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg		665	
Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg			
140	145	150	
gtc aag ctg ccc ggg aaa tgc tgt gag gag tgg gtg tgt gat gag ccc		713	
Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro			
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Lys Asp Arg Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu			
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gac aca ttt ggc cct gac cca act atg atg cga gcc aac tgc ctg gtc		809	
Asp Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val			
185	190	195	
cag acc aca gag tgg agc gcc tgt tct aag acc tgt ggg atg ggc atc		857	
Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile			
200	205	210	215
tcc acc cgg gtt acc aat gac aat acc ttc tgc agg ctg gag aag cag		905	
Ser Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln			
220	225	230	
agt cgt ctc tgc atg gtc agg ccc tgt gaa gct gac cta gag gaa aac		953	
Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn			
235	240	245	
att aag aag ggc aaa aag tgc atc cgg acg cct aaa att gcc aag cct		1001	
Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro			

250

255

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gtc aag ttt gag ctt tct ggc tgc acc agt gtg aag acc tac cgg gct		1049	
Val Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala			
265	270	275	
aag ttc tgt ggg gtg tgc acg gac ggc cgc tgc tgc aca ccg cac aga		1097	
Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg			
280	285	290	295
acc acc aca ctg ccg gtg gag ttc aag tgc ccc gat ggc gag atc atg		1145	
Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met			
300	305	310	
aaa aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt		1193	
Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys			
315	320	325	
ccc ggg gac aat gac atc ttt gag tcc ttg tac tac agg aag atg tat		1241	
Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr			
330	335	340	
gga gac atg gcg taa agccagggag taagggacac gaactcattt agactataac		1296	
Gly Asp Met Ala			
345			
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aagagtggag atgccaggag aaagacaggt actagctgag gtcattttaa aagcagcgat		1596	
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gcgaacaaat ggccttatt aagaaatggc ttgctcaggg taactggtca gattccacg		2196	
aggaagtgtt tgctgcttct ttgactatga ctgggttggg aggcaatttta tttgttggaa		2256	

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tatatgaaaa aaaaaaaaaa aa 2338

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<213> Rat

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Cys Ala Arg Glu Ala Ala Pro Arg Cys Pro Ala Gly Val Ser Leu Val  
35 40 45  
  
Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly Glu  
50 55 60  
  
Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe Cys  
65 70 75 80  
  
Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Pro Ala Lys  
85 90 95  
  
Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly Glu  
100 105 110  
  
Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly Ala  
115 120 125  
  
Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser Pro  
130 135 140  
  
Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu  
145 150 155 160  
  
Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Val Val Gly Pro Ala  
165 170 175  
  
Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr Met  
180 185 190  
  
Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys Ser  
195 200 205  
  
Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Thr  
210 215 220  
  
Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro Cys  
225 230 235 240  
  
Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg  
245 250 255

Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys Thr  
260 265 270

Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp Gly  
275 280 285

Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu Phe Lys  
290 295 300

Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys Thr  
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Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu Ser  
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1	5	10	15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag	96		
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys			
20	25	30	

cct ggg ggg tcc ctt aag acc tct cct gtg cag cct ctg gat tca act	144		
Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr			
35	40	45	

ttc agt aac gcc tgg atg agc tgg gtc cgc cag gct cca gga agg ggc	192		
Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly			
50	55	60	

tgg agt ggg ttg gcc gta tta aaa gca aaa ctg atg gtg gga cac aca	240		
Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr			
65	70	75	80

gac tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat	288		
Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp			
85	90	95	

tca aaa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gag gac	336		
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp			
100	105	110	

aca gcc gtg tat tac tgt acc aca aaa tgg gtg gct acg gac tac ttt	384		
Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe			
115	120	125	

gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc	432		
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr			
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aag ggc cca tcg	444		
Lys Gly Pro Ser			
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Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr  
35 40 45

Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly  
50 55 60

Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr  
65 70 75 80

Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp  
85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp  
100 105 110

Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe  
115 120 125

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Lys Gly Pro Ser  
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gcc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96  
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

cct	ggg	gcc	tca	gtg	aag	gtc	tcc	tgc	aag	gct	ttc	tgg	cta	cac	ctt	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Phe	Trp	Leu	His	Leu	
35						40						45				
tca	ccc	ggc	tac	tat	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	192
Ser	Pro	Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
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ctt	gag	tgg	atg	gga	tgg	atc	aac	cct	aat	agt	agt	ggc	aca	cac	tat	240
Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Ser	Gly	Thr	His	Tyr	
65					70					75			80			
gca	cag	atg	ttt	cag	ggc	agg	gtc	acc	gtg	acc	agg	gac	acg	tcc	atc	288
Ala	Gln	Met	Phe	Gln	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Ile	
85						90				95						
agc	aca	gcc	tac	atg	gag	ctg	agc	agg	ctg	aga	tct	gac	gac	acg	gcc	336
Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	
100					105					110						
gtg	tat	tac	tgt	gcg	aga	gag	ggg	ata	gca	gca	gct	gcc	atc	tac	ggt	384
Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Gly	Ile	Ala	Ala	Ala	Ile	Tyr	Gly		
115					120					125						
atg	gac	gtc	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	gcc	tcc	432
Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	
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Thr	Lys	Gly	Pro	Ser												
145																

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				20			25						30			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Phe	Trp	Leu	His	Leu	
				35			40					45				
Ser	Pro	Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	
				50			55			60						
Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Ser	Gly	Thr	His	Tyr	
				65			70			75			80			
Ala	Gln	Met	Phe	Gln	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Ile	
				85			90			95						
Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	

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Val Tyr Tyr Cys Ala Arg Glu Gly Ile Ala Ala Ala Ala Ile Tyr Gly		
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Thr Lys Gly Pro Ser		
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		15
acc cac gcc cag gtc cag ctg gta cag ttt ggg gct gag gtg aag aag		96
Thr His Ala Gln Val Gln Leu Val Gln Phe Gly Ala Glu Val Lys Lys		
20	25	30
cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc		144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu		
35	40	45
act gaa tta tcc atg cac tgg gtg cga cag gct cct gga aaa ggg ctt		192
Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
50	55	60
gag tgg atg gga agt ttt gat cct gaa gat ggt gaa aca atc tac gca		240
Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala		
65	70	75
80		
cag aag ttc cag ggc aga gtc acc atg acc gag gac aca tct aca gac		288
Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp		
85	90	95
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg		336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100	105	110

tat tac tgt gca acc tct acg gtg gta act ccg tgg tac ttt gac tac 384  
Tyr Tyr Cys Ala Thr Ser Thr Val Val Thr Pro Trp Tyr Phe Asp Tyr  
115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc 432  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
130 135 140

cca tcg 438  
Pro Ser  
145

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Thr His Ala Gln Val Gln Leu Val Gln Phe Gly Ala Glu Val Lys Lys  
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu  
35 40 45

Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala  
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Thr Ser Thr Val Val Thr Pro Trp Tyr Phe Asp Tyr  
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
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Pro Ser  
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1									10						15	

acc cac gcc cag gtc cag ctg gta cag tct ggg gct gag gtg aag aag 96  
 Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc 144  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu  
 35 40 45

act gaa tta tcc atg cac tgg gtg cga cag gct cct gga aaa ggg ctt 192  
 Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

gag tgg atg gga agt ttt gat cct gaa gat ggt gaa aca atc tac gca 240  
 Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala  
 65 70 75 80

cag aag ttc cag ggc aga gtc acc atg acc gag gac aca tct aca gac 288  
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp  
 85 90 95

aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

tat tac tgt gca acc tct acg gtg gta act ccg tgg tac ttt gac tac 384  
 Tyr Tyr Cys Ala Thr Ser Thr Val Val Thr Pro Trp Tyr Phe Asp Tyr  
 115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc 432  
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 130 135 140

cca tcg 438  
 Pro Ser  
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1									10						15	

Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu  
35 40 45

Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala  
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Thr Ser Thr Val Val Thr Pro Trp Tyr Phe Asp Tyr  
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
130 135 140

Pro Ser  
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1 5 10 15

ggt cct gtc cca ggt gca gct gca gga gtc ggg ccc agg act ggt gaa 96  
Gly Pro Val Pro Gly Ala Ala Gly Val Gly Pro Arg Thr Gly Glu  
20 25 30

gcc ttc aca gac cct gtc ctc acc tgc act gtc tct ggt ggc tcc atc 144  
Ala Phe Thr Asp Pro Val Leu Thr Cys Thr Val Ser Gly Gly Ser Ile  
35 40 45

agc agt ggt ggt tac tac tgg agc tgg atc cgc cag cac cca ggg aag 192  
Ser Ser Gly Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys  
50 55 60

ggc ctg gag tgg att ggg tac atc tat tac agt ggg agc acc tac tac 240  
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr  
65 70 75 80

aac ccg tcc ctc aag agt cga gtt acc ata tca gta gac acg tct aag 288  
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys  
85 90 95

aac cag ttc tcc ctg aag ctg agc tct gtg act gcc gcg gac acg gcc 336  
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110

gtg tat tac tgt gcg agc tat tac tat gat agt ggt ggt tat tac gac 384  
Val Tyr Tyr Cys Ala Ser Tyr Tyr Asp Ser Gly Gly Tyr Tyr Asp  
115 120 125

tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc 432  
Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala  
130 135 140

tcc acc aag ggc cca tcg 450  
Ser Thr Lys Gly Pro Ser  
145 150

<210> 14  
<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Lys His Leu Trp Phe Phe Leu Pro Ala Gly Gly Ser Ser Gln Met  
1 5 10 15

Gly Pro Val Pro Gly Ala Ala Gly Val Gly Pro Arg Thr Gly Glu  
20 25 30

Ala Phe Thr Asp Pro Val Leu Thr Cys Thr Val Ser Gly Gly Ser Ile  
35 40 45

Ser Ser Gly Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys  
50 55 60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr  
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys  
85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110

Val Tyr Tyr Cys Ala Ser Tyr Tyr Asp Ser Gly Gly Tyr Tyr Asp  
115 120 125

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala  
130 135 140

Ser Thr Lys Gly Pro Ser  
145 150

<210> 15  
<211> 423  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(423)

<220>  
<221> sig\_peptide  
<222> (1)..(60)

<220>  
<221> V\_region  
<222> (61)..(365)

<400> 15  
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48  
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96  
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag act 144  
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Thr  
35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192  
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240  
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288  
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agc ctg cag gct gac gat gtg gca gtt tat 336  
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr  
100 105 110

tac tgt cag caa tat tat agt act cct ccg tgg acg ttc ggc caa ggg 384  
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Trp Thr Phe Gly Gln Gly  
115 120 125

acc aag gtg gaa atc aaa cga act gtg gct gca cca tct 423

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser  
130 135 140

<210> 16  
<211> 141  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Thr  
35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr  
100 105 110

Tyr Cys Gln Gln Tyr Ser Thr Pro Pro Trp Thr Phe Gly Gln Gly  
115 120 125

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser  
130 135 140

<210> 17  
<211> 420  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(420)

<220>  
<221> sig\_peptide  
<222> (1)..(60)

<220>  
<221> V\_region  
<222> (61)..(364)

<400> 17  
atg aag gat ctg ctc agc ttc ctg ggg ctg cta atg ctc tgg ata cct 48  
Met Lys Asp Leu Leu Ser Phe Leu Gly Leu Leu Met Leu Trp Ile Pro

1	5	10	15	
gga tcc agt gca gat att gtc atg acc cag acg cca ctc ttc tgt ccg				96
Gly Ser Ser Ala Asp Ile Val Met Thr Gln Thr Pro Leu Phe Cys Pro				
20	25	30		
tca ccc ctg gac agc cga gcc tcc atc tcc tgc aag tct ggt ctg agc				144
Ser Pro Leu Asp Ser Arg Ala Ser Ile Ser Cys Lys Ser Gly Leu Ser				
35	40	45		
ctc ctg cac agt gat gga aag acc tat ttg cat tgg tac ctg cag aag				192
Leu Leu His Ser Asp Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys				
50	55	60		
cca ggc cag cct cca cag ctc ctg atc tat gag agt ttc caa ccg gtt				240
Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Ser Phe Gln Pro Val				
65	70	75	80	
ctc ctg gag tgc cag ata ggc tca gtg gca gcg ggt cag gac aga ttt				288
Leu Leu Glu Cys Gln Ile Gly Ser Val Ala Ala Gly Gln Asp Arg Phe				
85	90	95		
cac act gaa aat cag ccg ggt gga agg ctg agg aat gtt ggg gtt tat				336
His Thr Glu Asn Gln Pro Gly Gly Arg Leu Arg Asn Val Gly Val Tyr				
100	105	110		
tac tgc atgcaa agt tta cag ctt ccg ctc act ttc ggc gga ggg acc				384
Tyr Cys Met Gln Ser Leu Gln Leu Pro Leu Thr Phe Gly Gly Thr				
115	120	125		
aag gtg gag atc aaa cga act gtg gct gca cca tct				420
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser				
130	135	140		
<210> 18				
<211> 140				
<212> PRT				
<213> Homo sapiens				
<400> 18				
Met Lys Asp Leu Leu Ser Phe Leu Gly Leu Leu Met Leu Trp Ile Pro				
1	5	10	15	
Gly Ser Ser Ala Asp Ile Val Met Thr Gln Thr Pro Leu Phe Cys Pro				
20	25	30		
Ser Pro Leu Asp Ser Arg Ala Ser Ile Ser Cys Lys Ser Gly Leu Ser				
35	40	45		
Leu Leu His Ser Asp Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys				
50	55	60		
Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Ser Phe Gln Pro Val				
65	70	75	80	
Leu Leu Glu Cys Gln Ile Gly Ser Val Ala Ala Gly Gln Asp Arg Phe				
85	90	95		

His Thr Glu Asn Gln Pro Gly Gly Arg Leu Arg Asn Val Gly Val Tyr  
100 105 110

Tyr Cys Met Gln Ser Leu Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr  
115 120 125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser  
130 135 140

<210> 19

<211> 405

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(405)

<220>

<221> sig\_peptide

<222> (1)..(66)

<220>

<221> V\_region

<222> (67)..(353)

<400> 19

atg gac atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15

ctc tca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc ttc 96  
Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe  
20 25 30

cct gtc tgc atc tgt agg aga cag agt cac cat cac ttg cca ggc gag 144  
Pro Val Cys Ile Cys Arg Arg Gln Ser His His His Leu Pro Gly Glu  
35 40 45

tca gga cat tca cca cta ttt aaa ttg gta tca gca gaa acc agg gaa 192  
Ser Gly His Ser Pro Leu Phe Lys Leu Val Ser Ala Glu Thr Arg Glu  
50 55 60

agc cct aag ctc ctg atc tac gat gca tcc aat ttg gaa aca ggg tcc 240  
Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Ser  
65 70 75 80

cat cac ggt tca gtg gaa gtg gat ctg gga cag att tta ctt tca cca 288  
His His Gly Ser Val Glu Val Asp Leu Gly Gln Ile Leu Ser Pro  
85 90 95

tca gca gcc tgc agc tct gaa gat att gca aca tat tac tgt caa cag 336  
Ser Ala Ala Cys Ser Ser Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110

tat aat aat ctc atc acc ttc ggc caa ggg aca cga ctg gag att aaa 384  
Tyr Asn Asn Leu Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

115

120

125

405

cga act gtg gct gca cca tct  
Arg Thr Val Ala Ala Pro Ser  
130 135

<210> 20  
<211> 135  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15

Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe  
20 25 30

Pro Val Cys Ile Cys Arg Arg Gln Ser His His His Leu Pro Gly Glu  
35 40 45

Ser Gly His Ser Pro Leu Phe Lys Leu Val Ser Ala Glu Thr Arg Glu  
50 55 60

Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Ser  
65 70 75 80

His His Gly Ser Val Glu Val Asp Leu Gly Gln Ile Leu Leu Ser Pro  
85 90 95

Ser Ala Ala Cys Ser Ser Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110

Tyr Asn Asn Leu Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
115 120 125

Arg Thr Val Ala Ala Pro Ser  
130 135

<210> 21  
<211> 387  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(387)

<220>  
<221> sig\_peptide  
<222> (1)..(47)  
<223> Initiation codon and a portion of a signal sequence are lacked.

<220>  
<221> V\_region

<222> (48) .. (335)

<400> 21  
gat agg gtc cta ggg gtc ctg atg gtt ggg ttt tcg gtg ccg gat gag 48  
Asp Arg Val Leu Gly Val Leu Met Val Gly Phe Ser Val Pro Asp Glu  
1 5 10 15

aac atc cag atg acc cag tat cca tct ccc tgt ctg cat acc tgt agg 96  
Asn Ile Gln Met Thr Gln Tyr Pro Ser Pro Cys Leu His Thr Cys Arg  
20 25 30

aga cag agt cac cat cac ttg cca gag cga gct cag gac att cac cac 144  
Arg Gln Ser His His Leu Pro Glu Arg Ala Gln Asp Ile His His  
35 40 45

tat cta aat tgg tat cag cag aaa cca ggg aaa gcc cta agc tct gat 192  
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Leu Ser Ser Asp  
50 55 60

cta cga tgc atc caa ttt gga aac agg gtc cca tca cgg ttc agt gga 240  
Leu Arg Cys Ile Gln Phe Gly Asn Arg Val Pro Ser Arg Phe Ser Gly  
65 70 75 80

agt gga tct ggg aca gat tct act tca cca tca gca gcc tgc agc tct 288  
Ser Gly Ser Gly Thr Asp Ser Thr Ser Pro Ser Ala Ala Cys Ser Ser  
85 90 95

gaa gat att gca aca tat tac tgt caa cag tat aat aat ctc atc acc 336  
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Leu Ile Thr  
100 105 110

ttc ggc caa ggg aca cga ctg gag att aaa cga act gtg gct gca cca 384  
Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
115 120 125

tct 387  
Ser

<210> 22  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 22  
Asp Arg Val Leu Gly Val Leu Met Val Gly Phe Ser Val Pro Asp Glu  
1 5 10 15

Asn Ile Gln Met Thr Gln Tyr Pro Ser Pro Cys Leu His Thr Cys Arg  
20 25 30

Arg Gln Ser His His Leu Pro Glu Arg Ala Gln Asp Ile His His  
35 40 45

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Leu Ser Ser Asp  
50 55 60

Leu Arg Cys Ile Gln Phe Gly Asn Arg Val Pro Ser Arg Phe Ser Gly

65

70

75

80

Ser Gly Ser Gly Thr Asp Ser Thr Ser Pro Ser Ala Ala Cys Ser Ser  
 85 90 95

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Leu Ile Thr  
 100 105 110

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
 115 120 125

Ser

<210> 23  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(411)

<220>  
 <221> sig\_peptide  
 <222> (1)..(66)

<220>  
 <221> V\_region  
 <222> (67)..(356)

<400> 23  
 atg gac atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
 1 5 10 15

ctc tca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96  
 Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt 144  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45

cag agc att agc agc tat tta aat tgg tat cag cag aaa cca ggg aaa 192  
 Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60

gcc cct aag ctc ctg att tat gct gca tcc agt ttg caa agt ggg tcc 240  
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ser  
 65 70 75 80

cat caa ggt tca gtg gca gtg gat tat gcg aca gat ttc cat ttc tca 288  
 His Gln Gly Ser Val Ala Val Asp Tyr Ala Thr Asp Phe His Phe Ser  
 85 90 95

cca tca gca gtt tgc cac ctg acg att ttg caa ctt act act gtc cac 336  
 Pro Ser Ala Val Cys His Leu Thr Ile Leu Gln Leu Thr Thr Val His

100

105

110

aga gtt aca gta tcc cat tca ctt tcg gcc ctg ggg acc aaa gtg gat      384  
Arg Val Thr Val Ser His Ser Leu Ser Ala Leu Gly Thr Lys Val Asp  
115                          120                          125

agc aaa cga act gtg gct gca cca tct      411  
Ser Lys Arg Thr Val Ala Ala Pro Ser  
130                          135

<210> 24  
<211> 137  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
1                5                          10                          15

Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20                          25                          30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
35                          40                          45

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
50                          55                          60

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ser  
65                          70                          75                          80

His Gln Gly Ser Val Ala Val Asp Tyr Ala Thr Asp Phe His Phe Ser  
85                          90                          95

Pro Ser Ala Val Cys His Leu Thr Ile Leu Gln Leu Thr Thr Val His  
100                          105                          110

Arg Val Thr Val Ser His Ser Leu Ser Ala Leu Gly Thr Lys Val Asp  
115                          120                          125

Ser Lys Arg Thr Val Ala Ala Pro Ser  
130                          135

<210> 25  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
synthesized adaptor sequence

<220>  
<221> misc\_difference  
<222> (1)...(27)

<400> 25  
ccatcctaat acgactcact atagggc

27

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(25)

<400> 26  
ccagggccgc tgtgctctcg gaggt

25

<210> 27  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<220>  
<221> primer\_bind  
<222> (1)..(23)

<400> 27  
gggggtcagg ctggaactga gga

23